

Table S3. Origins of spacer sequences from coagulase negative staphylococci analyzed in this work.

Strain	Spacer*	Spacer sequence	Spacer origin, Genbank ID
<i>S. capitnis</i> CR01	scap01	CTAGATACCCAGAACAAAATAGGTCTAACGAAACAAT	unknown
	scap02	TCTATAAGTTCATTAATTCCGATACCTAGATTATCT	unknown
	scap03	AATTTCTAATTCTATAAGTTCATTAATTCCGAT	unknown
	scap04	TAATAGTGTGTTCTATTAAAAGATACAATCCTGT	unknown
	scap05	TAGAATGTTATTATCTAAGTGGTCGATGTATTCC	<i>Staphylococcus</i> phage phiPLA-RODI, KP027446.1
	scap06	CTTAAAATCTAATTGCATTGTTATCAATTCCCTTA	unknown
	scap07	TCTGTAATGTATTCTATTAATGTAATCATAATTTTTTC	unknown
	scap08	TAGACCATTACCTCATTATATTATAGTCTTATTAA	unknown
	scap09	TTTTCTTAACTGTTTTACTGCCCATTAATAGT	unknown
	scap10	ATAAACCCGTTCAATTGTTATCTTAAATTCTTG	unknown
	scap11	ACAACCTCGTCATCTTCATCATTTCTTACATCA	unknown
	scap12	ATATTCTTCATGAATAACACCCCTCCTTTTCTA	unknown
	scap13	AAGTTAACGGCATTACCTAATAAAAATTTTAGG	unknown
	scap14	TCATCTTCATGTCACTGATTAAATTCTATTGTA	unknown
	scap15	GGTAATAGTTGCTCAATAGTAATAAACGTCGGT	unknown
<i>S. capitnis</i> CR03	scap16	GCATAAAAGTTTGATATACACGATCGAATATGAGTT	unknown
	scap17	AGTGGTCCAGAATTAAATACATGGTAAAGGAGTATATCAGTT	unknown
	scap18	TGAAGACCAATTAGAATCATATCGCGCTTAGAAGAGTT	unknown
	scap19	CCTAAAATATTTTATTAGGTAATGCCGTTAATCT	unknown
	scap20	TGAAAAAAGGAGGGTGTATTATGGAAAGAAATA	unknown
	scap21	TGATGTAAGAGAAATGATGAAAGATGACGAAGTTG	unknown
	scap22	CAAGAATTAAAGATAACGAATTGAAACGGGTTA	unknown
	scap23	TAAGGAATTGATAACAATGCAATTAGATTAA	unknown
<i>S. epidermidis</i> RP62A	sepi01	GAGAATCAAGAAAAATGTTCACGACCGTACTAGTTCTCGT	unknown
	sepi02	TCGATGTAACGTATGCAAATGACAATTATTACTAGTTCTCGT	<i>Staphylococcus</i> phage PH15, DQ834250.1
	sepi03	TTTGTACTGATGATTATATACTTCGGCATACGTGTTCTCGT	<i>S. lugdunensis</i> plasmid pT33G-1, KU882683.1
<i>S. epidermidis</i> VCU037	sepi04	CTTGAAACTTACCAAACCATGGCTGACGATGT	<i>S. aureus</i> plasmid pGO400, KT780705.1
	sepi05	CAAGGCCATTAGTAGGTCGTAAAATGAAGTTAA	<i>S. pseudintermedius</i> plasmid pKM01, KT373969.1
	sepi06	TAGTAAGTGATTACATTATGACGGCATAGACGAACA	unknown
	sepi07	ATAAAAAAATTATTAAGGATATGATTGAAATG	unknown
	sepi08	GCGAAAAGAATTAAATAATTGTTGGCTTCAGAA	unknown
	sepi09	AGTCAATATAAGACAATACTTTACGCTTATATT	unknown
	sepi10	GCATTATATGTTAGATATTGTCACAGGTTTTT	unknown
	sepi11	TCTATCGTATTCCCTTAGTTCATCATTATTGTC	unknown
	sepi12	TGAATCATGTTCGCTACGTTCCGGCTTTCTT	unknown
	sepi13	TTTAATTGTTGCTCGATTGTTGGTTAAGCTAG	unknown
	sepi14	AATAAGGTCGAAACTGTTGGTAACTATCTTTA	unknown
	sepi15	AGATTTCCTTACGACTAAGACCTAAAATTCTTC	unknown
	sepi16	GCTCCTTTATATTTTATTGTCATTATTAA	unknown
	sepi17	CAATAATCCATTCTAATACATAATAATTAA	unknown

Table S3 (cont.). Origins of spacer sequences from coagulase negative staphylococci analyzed in this work.

Strain	Spacer*	Spacer sequence	Spacer origin, Genbank ID
<i>S. epidermidis</i> VCU037	sepi18	TAGTAATAATTGTCATTTGCATACGTTACATCGAT	unknown
	sepi19	TAGTACGGTCGTGAACATTTTCTTGATTCTCT	unknown
<i>S. haemolyticus</i> W75	shae01	TATTCAAAATAAAAGCCGACCTAAAAAG	unknown
	shae02	CGATTATCCATGATTTGGATATAAATT	unknown
	shae03	CCCTTATTCTTACTATCTAATATGTCTT	unknown
	shae04	TTCTAATTCACTATGGACTAGCGAATT	unknown
	shae05	CACTTCGGATAAATAAACCTACTCTA	unknown
	shae06	TAAGAGCATTATTAATTGATCTAGCATT	unknown
	shae07	GGCAGGTTACTGGTGTCCAGTGTCACT	unknown
	shae08	TGTACAACGAAGCAAATTGCTAATACAA	unknown
	shae09	AATCCGTCACCACATATTTGGTCTT	unknown
	shae10	AAACATGTACAAAGACAAAATAAAATTAT	<i>S. aureus</i> plasmid pUSA07-1-SUR24, CP014447.1
<i>S. lugdunensis</i> ACS-027-V-Sch2	shae11	CGACCGTGTATTTTAGTTGATGAACGTAT	unknown
	shae12	ATGTTGGTGTACACGACGCAAAGATGATA	unknown
	shae13	CATCTATATGGAATAGTCATCACAAACGTTA	unknown
	shae14	AAGAAGATATCATTGACTTGGTAGTGATT	unknown
	shae15	GATGAACAAAAAGAATCTATTACGGTAAG	unknown
	shae16	CCTCAGCACTTACAGTATCTTATTTCTT	<i>Staphylococcus</i> phage IME-SA4, KP735928.1
	shae17	TGCCCACTAGGTTGTTAGTTCTCGCTAAAGTC	unknown
	shae18	TATCGCTGCTAAACAATAAGGCGGTGTTGA	unknown
	shae19	AATCTGTAAGTTCTCTTGTAAATCAT	unknown
	shae20	TGAGCCTTAACAAACACTTCTGCTTGT	<i>S. aureus</i> pSAM12-0145, KU521355.1
<i>S. lugdunensis</i> HLU09-01	shae21	ATGATTGGATTGGTTAAGTTGGAATTA	<i>S. cohnii</i> plasmid pHK01, KC820816.1
	slug01	TCTTGCCTCCATAACATCTTAGCTAATTGGAACA	<i>S. aureus</i> plasmid pUR4128, JQ861960.1
	slug02	AGAAACAAACGGCGGATATGAGCATATAGAAATAT	unknown
	slug03	TAATGACACTTATGAATTGGTTAATAGAAATACAGAA	unknown
	slug04	TACAGTGATTTAATATGGAAAAGTACTGAGA	<i>S. aureus</i> plasmid pMI, AP017321.1
	slug05	TAATAAAGGAGTTTAACTATGTCAGTCTTAGATAAA	<i>S. epidermidis</i> plasmid SAP016A, GQ900381.1
	slug06	TTCTGTATTTCTATTAACCAATTCTACAGTGTCTT	<i>S. sciuri</i> plasmid pGFT2, AJ536194.1
	slug07	TTCATCATATCCTTTATATAGTTTGTGTT	unknown
	slug08	CCAGTTGCTATTTATTTGTCAACCATTAA	unknown
	slug09	TAGAATGTTAACAAAGGTGTTCAAACCTG	unknown
<i>S. lugdunensis</i> M23590	slug10	AACATTTATTCAGTCTGTTTGCCTCTACTAAGTAA	unknown
	slug11	TCGCTATTCAATAAGTTGTATTTGTCTCATT	unknown
<i>S. lugdunensis</i> N920143	slug12	AAACCATGCCAACAAAGCAATCCCTTATC	unknown
	slug13	ATAGAGATGAGAACGGTAATCTAATAGGTG	unknown
<i>S. lugdunensis</i> N920143	slug14	TAACACCTTGATTTATATCTTTCCATCAAAT	unknown
	slug15	CCAAATAATACTATTAATTATCTGTTAATGCTGTGG	unknown
	slug16	TGGTAAATCTCTACACTGTCGACTGGGTCTCTA	unknown

Table S3 (cont.). Origins of spacer sequences from coagulase negative staphylococci analyzed in this work.

Strain	Spacer*	Spacer sequence	Spacer origin, Genbank ID
<i>S. lugdunensis</i> N920143	slug17	TGTTCCAATTAGCTAAAGATGTTATGGACGGCAAGA	unknown
<i>S. massiliensis</i> CCUG55927	smas01	GACGTGGTTAGTTACTTACGCACATCAAT	unknown
	smas02	ATGCTCAAATAGAGTCGTGCAATCTTCCA	unknown
	smas03	GCCATCTAAAAATAATAGTGTGTT	unknown
	smas04	CAGAATAACCAGTTGTTGACCAGTTACA	unknown
	smas05	TCTTGATAACGCCCTTTCATCTGTTCATA	unknown
	smas06	TCTTGATAACGCCCTTTCATCTGTTCATA	unknown
	smas07	TCTTGATAACGCCCTTTCATCTGTTCATA	unknown
	smas08	GCATCTATTAGGTTAACGAAACCGGATGCC	unknown
	smas09	TGTCGATAAGTTTATTGTTGTCATT	unknown
<i>S. schleiferi</i> 1360-13	ssch01	CATAAATGTAATTAAATATCCTATCTTCTTG	unknown
	ssch02	CCCCATCAAACGAGCCATTTCATCTTGCCT	unknown
	ssch03	GCTCACACCTCCTAAAAACCAAATTCA	unknown
	ssch04	TTTACATCAGGTTGAATTAGTAGTTGCC	unknown
	ssch05	CGTAAATAACACAACCTCGCGTCCACCATC	unknown
	ssch06	CAGTTCTATATGTGATTTCTCTATCC	<i>S. aureus</i> plasmid p140355, KY465818.1, <i>S. xylosus</i> plasmid pSX01, KP890694.1 <i>S. epidermidis</i> plasmid pSP01, KR230047.1 <i>S. schleiferi</i> 1360-13, CP009470.1 unknown
	ssch07	CCAAAGCTACCTTAATTCCATGTTCTC	unknown
	ssch08	AAAAACGTAGGCAATGTAATGGTTGTTGAA	unknown
	ssch09	TAAATTCAAACTTATATTTGAGGTTCTGC	<i>S. epidermidis</i> plasmid p14-01514, KX520649.1 <i>S. aureus</i> plasmid pSAM12-0145, KU521355.1 <i>S. cohnii</i> plasmid pHK01, KC820816.1 unknown
	ssch10	GCTGTTGCTATCTATTCACTAACTCTTTA	unknown
	ssch11	TTAAATGCATTTAATAAAAACCAATATT	unknown
	ssch12	CAGCCACGTATGTTAACAGTGAATGTT	unknown
	ssch13	AGGTGATATTGGAGTTGGTATTCTAATA	unknown
	ssch14	CTGTATCGTATGGATAATAAAACTTTCG	unknown
	ssch15	AAATGTTGCAAGGTGTTGAAGCAATGGCCG	unknown
	ssch16	TACAACAAGGTTCTAAAGAAGCTAGAGAAG	unknown
	ssch17	CAGCTTCAGGCGCTTCATGTTGCTTCTT	unknown
	ssch18	CGGCAAAAGCAATCATAGGGGGTGCAAAAT	unknown
	ssch19	TAAATCTTTCCATCAAATCTTAAATAC	unknown
	ssch20	ATACCCTACTGAGGATGAATGGACAGAAGT	unknown
	ssch21	TGGCGCGAATTACGGCGGTGGATACGGTCA	unknown
	ssch22	CTTCGTTTGCTTGTAGCTTCAAACATTA	unknown
	ssch23	GTCATTGATGTCTAAGTAACCTTCTTCTGA	unknown
	ssch24	TGTTAAAGTAAAGTTGTCTTGTGATT	unknown
	ssch25	GCAACGATTGTCGGAAGAGAAGATAATCG	unknown
	ssch26	AAAGAGACGGAAATGGATATGTAAGGATTA	unknown
	ssch27	GAACGCAGAAAAGAACACGCCATAAGGTGC	unknown
	ssch28	CGTCGTGAATAATAGTGTCTTATTATTCG	unknown

Table S3 (cont.). Origins of spacer sequences from coagulase negative staphylococci analyzed in this work.

Strain	Spacer*	Spacer sequence	Spacer origin, Genbank ID
S. schleiferi 2142-05	ssch29	TGTTTCAATACCGAATTATGAAGTGGTAT	unknown
	ssch30	GAGGTTGACCTGTACTCTTCTATGTCGT	<i>Staphylococcus</i> phage SpT252, KX827370.1
	ssch31	ATAGTGGCATGATAGGTTCAAGTGTCCCTT	unknown
	ssch32	AGACTGGCGATGGTCTCGCTTAAATACGTT	unknown
	ssch33	CAGGTATAGCGCGTATAGATAACCTTTCTT	unknown
	ssch34	CGCCCCTCTAAAGATAATTGATTCCCTCT	unknown
	ssch35	AAATAAAAATAGCTTAATTAAATGGCTATTT	unknown
	ssch36	CATAAGCGACAGACTGTTGTTGATTTCAT	unknown
	ssch37	TATCATAGAACAGAGGATGACAGCTGGGT	unknown
	ssch38	GGGCTACTAATCTTTGAACCTGCATAGT	unknown
	ssch39	CTTCCTCTGTCGTTCCCTCCTGTCACTTG	unknown
	ssch40	TTGTGATTCTTATTTGTCCGTATAATCT	unknown
	ssch41	AATGGCTTACATTAACAAATTCAACGAAAT	unknown
S. schleiferi 2317-03	ssch42	GTGTAACTCCTACTTGATTGCAACACTCA	unknown
	ssch43	GGGCTACTAATCTTTGAACCTGCATAGT	unknown
	ssch44	TTGTGATTCTTATTTGTCCGTATAATCT	unknown
	ssch45	ACCAGCCACCAGGTTGGAACAGATAACCTCA	unknown
	ssch46	GGATTTGCCCAACAACGACTAGCCAGT	unknown
	ssch47	ACCAGCCACCAGGTTGGAACAGATAACCTCA	unknown
	ssch48	GAATTCTTCTCTGTAACAAATCCGCGCT	unknown
	ssch49	GTGTTACCTTCTCTGTTCTAATAACTTAT	unknown
	ssch50	TTAGTTCAAGGTCTAAAGACGTAAATGCAGTA	unknown
	ssch51	AACGTATCCACCATAATTATTTTACATT	unknown
	ssch52	CTACTTACCGCAATCAGAAGTTAATATTG	unknown
	ssch53	CTAAACCTAAATAGTTTAGCAAGTTCAA	unknown
	ssch54	TGATCAGCTCAAATTCAAGTTCCACCGT	unknown
S. schleiferi 5909-02	ssch55	TAGTTTTCCACCTGAAATCTATTTTTG	unknown
	ssch56	TCTTTATCATGTTAAAGTTGAGAATACA	Phage 2638A, AY954954.1
	ssch57	CTAACAAATGTGAATATACGTCTAAAGTTG	unknown
	ssch58	TAGTTTTTATGGTCTGTAATCACCTTA	unknown
	ssch59	GTGGAATTGTAGCAATCTTATTAGGTCTTG	unknown
	ssch60	AATGGCTTACATTAACAAATTCAACGAAAT	unknown
	ssch61	GTGGAACCTACTTGATTGCAACACTCA	unknown
	ssch62	GGGCTACTAATCTTTGAACCTGCATAGT	unknown
	ssch63	ACCAGCCACCAGGTTGGAACAGATAACCTCA	unknown
	ssch64	GAATTCTTCTCTGTAACAAATCCGCGCT	unknown
	ssch65	TAGTGCCATTCTAAATAGTTCGAACCCA	unknown
	ssch66	TGATACGCATAATACAAATCCTTACCTAAAA	unknown
	ssch67	ATAGGCATACACCCGTAATCAAATTGATA	unknown
S. schleiferi 5909-02	ssch68	GAAGAGATCTCAAGGTTTTAAAGATGAG	unknown
	ssch69	TAGGATAACCTTGTAAAGAATTATGTTT	unknown
	ssch70	ATCAGTTGCCTCTTGTATCGTAAACAA	unknown
	ssch71	TCTTTATCATGTTAAAGTTGAGAATACA	Phage 2638A, AY954954.1
	ssch72	CTAACAAATGTGAATATACGTCTAAAGTTG	unknown

Table S3 (cont.). Origins of spacer sequences from coagulase negative staphylococci analyzed in this work.

Strain	Spacer*	Spacer sequence	Spacer origin, Genbank ID
S. schleiferi TSCC54	ssch73	TAGTTTTTATGGCTGTAATCACCTTA	unknown
	ssch74	GTGGAATTGTAGCAATCTTATTAGGTCTG	unknown
	ssch75	AATGGCTTACATTAACAAATTCAACGAAAT	unknown
	ssch76	CCAACAACAAATAGTACCATAGGTGTTTC	unknown
	ssch77	GTGTAACTCCTACTTGATTGCAACACTCA	unknown
	ssch78	ACTTCTCTGCCATTCTGCTAATTGTTCTACTTTG	unknown
	ssch79	ACTAGATACCCAGAACAAAATAGGTCAACGAAA	unknown
	ssch80	TCTATAAGTTCTTAAATTCCGATACCTAGATTCT	unknown
	ssch81	TTTTTCCACCCCTTCAGATCATCTATGATCTTG	unknown
	ssch82	AATTCTCTAAATTCTATAAGTTCTTAAATTCCGAT	unknown
	ssch83	TATACTATTACATAATTTTATGTGTCTGTCTAC	unknown
	ssch84	TAATAGTGTGTTCTCTATTAAAAGATACAATCCTGT	unknown
	ssch85	TCTGTAATGTATTCTTAAATGTAATCATAATTTC	unknown
	ssch86	TAGACCATTACCTCATTATATTATAGTCTTATT	unknown
	ssch87	TTTCTTAACTGTTTACTGCCATTAAAGT	unknown
	ssch88	ATAAACCGGTTCAATTGTTATCTTAAATTCTG	unknown
	ssch89	ACAACCTCGCATTTTCATCATTCTCTACATCA	unknown
	ssch90	ATATTCTTCCATGAATAACACCCCTCTTTCTA	unknown
	ssch91	AAGTTAACGGCATTACCTAATAAAATATTAGG	unknown
	ssch92	TCATCTTCATGTCACTGATTAATTCTATTGTA	unknown
	ssch93	GGTAATAGTTGCTCAATAGGTAAATAACGTCGGT	unknown
	ssch94	CTTCTAACGCGATATGATTCTAATTGGCTTCA	unknown
	ssch95	GATATACTCCTTACCATGTATTAAATTCTGGACCACT	unknown
	ssch96	CATATTGATCGTGTATATCAAACCTTATGC	unknown
	ssch97	CTTCCGAATCCATTTCAGCGCAATAAACAA	unknown
	ssch98	GATTGATAGTTGCGATTCTGCAGTCATT	unknown
	ssch99	ACTCACTGTAAATTCCCTCACTTGCTCTA	unknown
	ssch100	TCGTCATCAATCCATGCCATATGCTTCTT	unknown
	ssch101	TGACAACCACGCTTTAGCTTGCATATCAA	unknown
	ssch102	ATATTCTATTCAATTGTTCTGCAACTTGT	unknown
	ssch103	TTACATAATCGTTATGATTATTCTATGTT	unknown
	ssch104	CTGGAATAACCACAAAGCCAGAGTCAGTT	unknown
	ssch105	CCATGATGTCTAAAACACCGATTACCAT	unknown
	ssch106	ACGTTAGATTGCGAGGTGTTAACGACGGCT	unknown
	ssch107	TGTATGGGTGCGGTGACTCTACTATCA	unknown
	ssch108	GTAAATAATTCCGTTGGACTCGTTACGTT	unknown
	ssch109	CCATCGCTTCTTGCCTGAATTGAAATAT	unknown
	ssch110	ATGTTTTTCATTAAAGCTACCAAGTAATT	unknown
	ssch111	AATTCCGCTTATATTCAAGTTCTTTTT	unknown
S. simulans FDAARGOS_124	ssim01	CTTTCTAGTGCTAACTGCGTGTATTATC	unknown
	ssim02	CAAAAGAACGTATTAATGGAAAACAATTA	unknown
	ssim03	TAGTGACAACAAAGCGAAAATCGAGATTA	unknown
	ssim04	AAGTGGCGACAAGTATTGAAAATTGCA	unknown
	ssim05	AAGTGGCGACAAGTATTAAAAATTGCA	unknown
	ssim06	AGCGGAAACCCGATTGATTAAGCAAAG	unknown

Table S3 (cont.). Origins of spacer sequences from coagulase negative staphylococci analyzed in this work.

Strain	Spacer*	Spacer sequence	Spacer origin, Genbank ID
S. warner 691_SWAR	ssim07	GATGCATCAAATGTTTACGCCAATTCA	unknown
	ssim08	TGTGACTTACCTAAATCTAACATTGATAT	unknown
	ssim09	ATTACGGAGGATGTCATCGGCTTCTAACAA	unknown
	ssim10	AAGTTTGTTGTTCATGATAACAGGAAA	unknown
	ssim11	TGTTTAAATGCTCTAAAGAAAGTGCTT	unknown
	ssim12	ATGAACCTAAATCAGTGATAAGCGATT	unknown
	ssim13	CAAGGTGAGCGTGTTATCCGAACAAAAAG	unknown
	ssim14	TTGAACATATATGAAAGCTACTGTAACCC	unknown
	ssim15	TTGTAGCATAACAACAAACTGTGCTCTAA	unknown
	ssim16	AAAGCAGTATGAATGCAACAAACAAAATCCT	unknown
	ssim17	AAAGTAATATCAATACAAATCGTATGGCAA	unknown
	ssim18	ATTAAGTTAGGCTTGCAGATGAGAAATCA	unknown
	swar01	GTGAAACATATCAAATGCTTAACCTAGGTAAATATC	unknown
	swar02	GTGAAACTCCTGCATACGAAAATACTCAATCAGTGC	unknown
	swar03	GTGAAACGCTTTGAAAAATACAACGTAAAGCTTTA	unknown

*Some spacer sequences are identical: ssim04=ssim05, scap13=ssch91, scap03=ssch82, scap11=ssch89, scap45=scap47=ssch63, scap12=ssch90, scap15=ssch93, scap04=ssch84, scap08=ssch86, ssch58=ssch73, scap14=ssch92, scap02=ssch80, scap07=ssch85, scap03=ssch93, scap09=ssch87, ssch41=ssch60, ssch57=ssch72, ssch59=ssch74, ssch42=ssch77, ssch56=ssch71, ssch40=ssch44, ssch48=ssch64, ssch59=ssch74, ssch38=ssch43=ssch62, smas05=smas06=sma07. Total of unique sequences:194.